LISTING OF THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the application.

1. (Previously amended) A method for identification of a pathogenic organism from a predetermined group of pathogens, comprising:
   a) at least partially purifying nucleic acid from a clinical sample to create a clinical specimen,
   b) subjecting at least a first aliquot of said clinical specimen to at least a first amplification and detection reaction in one reaction vessel comprising:
      ba) at least a first set of amplification primers capable of amplifying a pre-selected nucleic acid sequence comprising the 16s/23s or 18s/26s rRNA spacer region from several or all members of said predetermined group of pathogens, wherein said predetermined group of pathogens comprises members of two or more genera,
      bb) at least one internal control template, and
      bc) a plurality of hybridization reagents, wherein the hybridization reagents comprise SEQ ID NOS: 3, 4, 5, 8, 9, 12 and 13,
      said reagents together being capable of specifically detecting a pre-selected nucleic acid sequence comprising the 16s/23s or 18s/26s rRNA spacer region from all members of said predetermined group of pathogens, further comprising a hybridization reagent capable of specifically detecting said internal control template; further comprising:
         bca) monitoring hybridization of each of said hybridization reagents at a pre-selected temperature, said hybridization being indicative of at least the genus of said pathogenic organism present in the sample, and
         bcb) monitoring temperature dependence of hybridization, said temperature dependence being indicative of at least the species of said pathogenic organism,

   wherein said amplification and detection reaction is indicative of the identity of said pathogenic organism from said predetermined group of pathogens.

2. (Previously amended) Method according to claim 1, further comprising subjecting at least a second aliquot of said clinical specimen to at least a second amplification and detection reaction in a different reaction vessel from said first aliquot of said clinical specimen being subjected to said first amplification and detection reaction.

3. (Previously amended) Method according to claim 2, further comprising subjecting at least a third aliquot of said clinical specimen to at least a third amplification and detection reaction in a different reaction vessel from said first aliquot of said clinical specimen being subjected to said first amplification and detection reaction, and said second aliquot of said clinical specimen being subjected to said second amplification and detection reaction.

4. (Canceled)

5. (Previously amended) Method according to claim 2, wherein gram positive pathogenic organisms are exclusively identified by said first amplification and detection reaction, and gram negative pathogenic organisms are exclusively identified by said second amplification and detection reaction.

6. (Previously amended) Method according to claim 3, wherein fungal pathogens are exclusively identified in said third amplification and detection reaction.

7. (Previously amended) Method according to claim 2, wherein said first amplification and detection reaction and said second amplification and detection reaction are performed with the same thermocycling profile.

8. – 9. (Canceled)